



RAW SEQUENCE LISTING

DATE: 07/25/2002

PATENT APPLICATION: US/09/686,647

TIME: 14:30:35

Input Set : N:\Crf3\RULE60\09686647.raw

Output Set: N:\CRF3\07252002\I686647.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
 5 (i) APPLICANT: THE ROCKEFELLER UNIVERSITY
 7 (ii) TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
 8 ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES
 THEREOF
 10 (iii) NUMBER OF SEQUENCES: 38
 12 (iv) CORRESPONDENCE ADDRESS:
 13 (A) ADDRESSEE: Klauber & Jackson
 14 (B) STREET: 411 Hackensack Avenue
 15 (C) CITY: Hackensack
 16 (D) STATE: New Jersey
 17 (E) COUNTRY: USA
 18 (F) ZIP: 07601
 20 (v) COMPUTER READABLE FORM:
 21 (A) MEDIUM TYPE: Floppy disk
 22 (B) COMPUTER: IBM PC compatible
 23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
 26 (vi) CURRENT APPLICATION DATA:
 C--> 27 (A) APPLICATION NUMBER: US/09/686,647
 C--> 28 (B) FILING DATE: 10-Oct-2000
 38 (C) CLASSIFICATION:
 31 (vii) PRIOR APPLICATION DATA:
 33 (A) APPLICATION NUMBER: US/09/183,374
 34 (B) FILING DATE:
 36 (A) APPLICATION NUMBER: 08/347,563
 37 (B) FILING DATE:
 40 (viii) ATTORNEY/AGENT INFORMATION:
 41 (A) NAME: Jackson Esq., David A.
 42 (B) REGISTRATION NUMBER: 26,742
 43 (C) REFERENCE/DOCKET NUMBER: 600-1-087 CIP
 45 (ix) TELECOMMUNICATION INFORMATION:
 46 (A) TELEPHONE: 201 487-5800
 47 (B) TELEFAX: 201 343-1684
 48 (C) TELEX: 133521
 51 (2) INFORMATION FOR SEQ ID NO: 1:
 53 (i) SEQUENCE CHARACTERISTICS:
 54 (A) LENGTH: 2793 base pairs
 55 (B) TYPE: nucleic acid
 56 (C) STRANDEDNESS: double
 57 (D) TOPOLOGY: linear
 59 (ii) MOLECULE TYPE: DNA (genomic)
 60 (A) DESCRIPTION: Murine ob cDNA

ENTERED

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62      (iii) HYPOTHETICAL: NO
64      (iv) ANTI-SENSE: NO
66      (vi) ORIGINAL SOURCE:
67          (A) ORGANISM: Murine
68      (ix) FEATURE:
69          (A) NAME/KEY: CDS
70          (B) LOCATION: 57..560
73      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
75 GGATCCCTGC TCCAGCAGCT GCAAGGTGCA AGAAGAAGAA GATCCCAGGG AGGAAA           56
77 ATG TGC TGG AGA CCC CTG TGT CGG TTC CTG TGG CTT TGG TCC TAT CTG           104
78 Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu
79   1      5      10      15
81 TCT TAT GTT CAA GCA GTG CCT ATC CAG AAA GTC CAG GAT GAC ACC AAA           152
82 Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
83      20      25      30
85 ACC CTC ATC AAG ACC ATT GTC ACC AGG ATC AAT GAC ATT TCA CAC ACG           200
86 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
87      35      40      45
89 CAG TCG GTA TCC GCC AAG CAG AGG GTC ACT GGC TTG GAC TTC ATT CCT           248
90 Gln Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro
91      50      55      60
93 GGG CTT CAC CCC ATT CTG AGT TTG TCC AAG ATG GAC CAG ACT CTG GCA           296
94 Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala
95      65      70      75      80
97 GTC TAT CAA CAG GTC CTC ACC AGC CTG CCT TCC CAA AAT GTG CTG CAG           344
98 Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln
99      85      90      95
101 ATA GCC AAT GAC CTG GAG AAT CTC CGA GAC CTC CTC CAT CTG CTG GCC           392
102 Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala
103      100      105      110
105 TTC TCC AAG AGC TGC TCC CTG CCT CAG ACC AGT GGC CTG CAG AAG CCA           440
106 Phe Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro
107      115      120      125
109 GAG AGC CTG GAT GGC GTC CTG GAA GCC TCA CTC TAC TCC ACA GAG GTG           488
110 Glu Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val
111      130      135      140
113 GTG GCT TTG AGC AGG CTG CAG GGC TCT CTG CAG GAC ATT CTT CAA CAG           536
114 Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln
115      145      150      155      160
117 TTG GAT GTT AGC CCT GAA TGC TGA AGTTTCAAAG GCCACCAGGC TCCCAAGA           588
118 Leu Asp Val Ser Pro Glu Cys
119      165
121 ATCATGTAGA GGGAAGAAAC CTTGGCTTCC AGGGGTCTTC AGGAGAAGAG AGCCATGTGC           648
123 ACACATCCAT CATTCAATTC TCTCCCTCCT GTAGACCACC CATCCAAAGG CATGACTCCA           708
125 CAATGCTTGA CTCAAGTTAT CCACACAAC TCAATGAGCAC AAGGAGGGGC CAGCCTGCAG           768
127 AGGGGACTCT CACCTAGTTC TTCAGCAAGT AGAGATAAGA GCCATCCCAT CCCCTCCATG           828
129 TCCCACCTGC TCCGGGTACA TGTTCTCCCG TGGGTACACG CTTGCTGCG GCCCAGGAGA           888
131 GGTGAGGTAG GGATGGGTAG AGCCTTTGGG CTGTCTCAGA GTCTTTGGGA GCACCGTGAA           948
133 GGCTGCATCC ACACACAGCT GGAAACTCCC AAGCAGCACA CGATGGAAGC ACTTATTTAT           1008

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135 TTATTCTGCA TTCTATTTTG GATGGATCTG AAGCAAGGCA TCAGCTTTTT CAGGCTTTTG 1068
137 GGGTCAGCCA GGATGAGGAA GGCTCCTGGG GTGCTGCTTT CAATCCTATT GATGGGTCTG 1128
139 CCCGAGGCAA ACCTAATTTT TGAGTGACTG GAAGGAAGGT TGGGATCTTC CAAACAAGAG 1188
141 TCTATGCAGG TAGCGCTCAA GATTGACCTC TGGTGACTGG TTTTGTCTCT ATTGTGACTG 1248
143 ACTCTATCCA AACACGTTTG CAGCGGCATT GCCGGGAGCA TAGGCTAGGT TATTATCAAA 1308
145 AGCAGATGAA TTTTGTCAAG TGTAATATGT ATCTATGTGC ACCTGAGGGT AGAGGATGTG 1368
147 TTAGAGGGAG GGTGAAGGAT CCGGAAGTGT TCTCTGAATT ACATATGTGT GGTAGGCTTT 1428
149 TCTGAAAGGG TGAGGCATTT TCTTACCTCT GTGGCCACAT AGTGTGGCTT TGTGAAAAGG 1488
151 ACAAAGGAGT TGACTCTTTC CGGAACATTT GGAGTGTACC AGGCACCCTT GGAGGGGCTA 1548
153 AAGCTACAGG CCTTTTGTTG GCATATTGCT GAGCTCAGGG AGTGAGGGCC CCACATTTGA 1608
155 GACAGTGAGC CCCAAGAAAA GGGTCCCTGG TGTAGATCTC CAAGGTTGTC CAGGGTTGAT 1668
157 CTCACAATGC GTTTCTTAAG CAGGTAGACG TTTGCATGCC AATATGTGGT TCTCATCTGA 1728
159 TTGGTTCATC CAAAGTAGAA CCCTGTCTCC CACCCATTCT GTGGGGAGTT TTGTTCCAGT 1788
161 GGAATGAGA AATCACTTAG CAGATGGTCC TGAGCCCTGG GCCAGCACTG CTGAGGAAGT 1848
163 GCCAGGGCCC CAGGCCAGGC TGCCAGAATT GCCCTTCGGG CTGGAGGATG AACAAAGGGG 1908
165 CTTGGGTTTT TCCATCACCC CTGCACCCTA TGTCACCATC AAAGTGGGGG GCAGATCAGT 1968
167 GAGAGGACAC TTGATGGAAG GCAATACACT TTAAGACTGA GCACAGTTTC GTGCTCAGCT 2028
169 CTGTCTGGTG CTGTGAGCTA GAGAAGCTCA CCACATACAT ATAAAAATCA GAGGCTCATG 2088
171 TCCCTGTGGT TAGACCCTAC TCGCGGCGGT GTACTCCACC ACAGCAGCAC CGCACCCTG 2148
173 GAAGTACAGT GCTGTCTTCA ACAGGTGTGA AAGAACCTGA GCTGAGGGTG ACAGTGCCCA 2208
175 GGGGAACCCCT GCTTGACGTC TATTGCATTT ACATACCGCA TTTCAGGGCA CATTAGCATC 2268
177 CACTCCTATG GTAGCACACT GTTGACAATA GGACAAGGGA TAGGGGTTGA CTATCCCTTA 2328
179 TCCAAAATGC TTGGGACTAG AAGAGTTTTG GATTTTAGAG TCTTTTCAGG CATAGGTATA 2388
181 TTTGAGTATA TATAAAATGA GATATCTTGG GGATGGGGCC CAAGTATAAA CATGAAGTTC 2448
183 ATTTATATTT CATAATACCG TATAGACACT GCTTGAAGTG TAGTTTTATA CAGTGTTTTA 2508
185 AATAACGTTG TATGCATGAA AGACGTTTTT ACAGCATGAA CCTGTCTACT CATGCCAGCA 2568
187 CTCAAAAACC TTGGGGTTTT GGAGCAGTTT GGATCTTGGG TTTTCTGTTA AGAGATGGTT 2628
189 AGCTTATACC TAAACCATA ATGGCAAACA GGCTGCAGGA CCAGACTGGA TCCTCAGCCC 2688
191 TGAAGTGTGC CCTTCCAGCC AGGTCATACC CTGTGGAGGT GAGCGGGATC AGGTTTTGTG 2748
193 GTGCTAAGAG AGGAGTTGGA GGTAGATTTT GGAGGATCTG AGGGC 2793

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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(A) DESCRIPTION: Murine ob polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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207 Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu
208 1 5 10 15
210 Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
211 20 25 30
213 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
214 35 40 45
216 Gln Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro
217 50 55 60
219 Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala
220 65 70 75 80
222 Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln

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223          85          90          95
225 Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala
226          100          105          110
228 Phe Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro
229          115          120          125
231 Glu Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val
232          130          135          140
234 Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln
235 145          150          155          160
237 Leu Asp Val Ser Pro Glu Cys
238          165
241 (2) INFORMATION FOR SEQ ID NO: 3:
243   (i) SEQUENCE CHARACTERISTICS:
244       (A) LENGTH: 700 base pairs
245       (B) TYPE: nucleic acid
246       (C) STRANDEDNESS: double
247       (D) TOPOLOGY: linear
249   (ii) MOLECULE TYPE: cDNA
250       (A) DESCRIPTION: Human ob cDNA where N represents any nucleotide
252   (iii) HYPOTHETICAL: NO
254   (iv) ANTI-SENSE: NO
256   (vi) ORIGINAL SOURCE:
257       (A) ORGANISM: Human
259   (ix) FEATURE:
260       (A) NAME/KEY: CDS
261       (B) LOCATION: 46..546
264   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
266 NNNNGNNGTTG CAAGGCCCAA GAAGCCCAN NTCCTGGGAA GGAAA ATG CAT TGG      54
267                               Met His Trp
268                               1
270 GGA ACC CTG TGC GGA TTC TTG TGG CTT TGG CCC TAT CTT TTC TAT GTC      102
271 Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu Phe Tyr Val
272   5          10          15
274 CAA GCT GTG CCC ATC CAA AAA GTC CAA GAT GAC ACC AAA ACC CTC ATC      150
275 Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile
276 20          25          30          35
278 AAG ACA ATT GTC ACC AGG ATC AAT GAC ATT TCA CAC ACG CAG TCA GTC      198
279 Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val
280          40          45          50
282 TCC TCC AAA CAG AAA GTC ACC GGT TTG GAC TTC ATT CCT GGG CTC CAC      246
283 Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His
284          55          60          65
286 CCC ATC CTG ACC TTA TCC AAG ATG GAC CAG ACA CTG GCA GTC TAC CAA      294
287 Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln
288          70          75          80
290 CAG ATC CTC ACC AGT ATG CCT TCC AGA AAC GTG ATC CAA ATA TCC AAC      342
291 Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile Ser Asn
292          85          90          95
294 GAC CTG GAG AAC CTC CGG GAT CTT CTT CAC GTG CTG GCC TTC TCT AAG      390

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295 Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys
296 100 105 110 115
298 AGC TGC CAC TTG CCC TGG GCC AGT GGC CTG GAG ACC TTG GAC AGC CTG 438
299 Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu
300 120 125 130
302 GGG GGT GTC CTG GAA GCT TCA GGC TAC TCC ACA GAG GTG GTG GCC CTG 486
303 Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu
304 135 140 145
306 AGC AGG CTG CAG GGG TCT CTG CAG GAC ATG CTG TGG CAG CTG GAC CTC 534
307 Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu
308 150 155 160
310 AGC CCT GGG TGC TGAGGCCTT GAAGGTCCTT CTCCTGCAA GGACTNACGT 585
311 Ser Pro Gly Cys
312 165
314 TAAGGGAAGG AACTCTGGTT TCCAGGTATC TCCAGGATTG AAGAGCATTG CATGGACACC 645
316 CCTTATCCAG GACTCTGTCA ATTTCCCTGA CTCCTCTAAG CCACTCTTCC AAAGG 700
319 (2) INFORMATION FOR SEQ ID NO: 4:
321 (i) SEQUENCE CHARACTERISTICS:
322 (A) LENGTH: 167 amino acids
323 (B) TYPE: amino acid
324 (D) TOPOLOGY: linear
326 (ii) MOLECULE TYPE: protein
327 (A) DESCRIPTION: Human ob polypeptide
329 (vi) ORIGINAL SOURCE:
331 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
333 Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu
334 1 5 10 15
336 Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
337 20 25 30
339 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
340 35 40 45
342 Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro
343 50 55 60
345 Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala
346 65 70 75 80
348 Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln
349 85 90 95
351 Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala
352 100 105 110
355 Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu
356 115 120 125
359 Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val
360 130 135 140
362 Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln
363 145 150 155 160
366 Leu Asp Leu Ser Pro Gly Cys
367 165
370 (2) INFORMATION FOR SEQ ID NO: 5:
372 (i) SEQUENCE CHARACTERISTICS:

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/686,647

DATE: 07/25/2002

TIME: 14:30:36

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Output Set: N:\CRF3\07252002\I686647.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:501 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8
L:521 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9
L:563 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11
L:643 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=13
L:665 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=14
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L:709 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=16
L:824 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=21
L:1112 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=29
L:1131 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=30
L:1152 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=31
L:1173 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=32
L:1195 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=33
L:1215 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=34
L:1236 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=35
L:1257 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=36
L:1278 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=37